Exhibit A

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CC   contiguous amino acids. The new human Ras-like proteins and the
CC   polypeptides encoding them are useful in the diagnosis, prevention, and
CC   treatment of inflammation and disorders associated with cell
CC   proliferation and apoptosis. They are also useful in treating AIDS and
CC   other infectious or genetic immunodeficiencies, neurodegenerative
CC   diseases (Alzheimer's disease, Parkinson's disease, amyotrophic lateral
CC   sclerosis, retinitis pigmentosa, cerebellar degeneration), aplastic
CC   anaemia, ischemic injuries (myocardial infarction, stroke), toxin-induced
CC   diseases (alcohol-induced liver damage, cirrhosis, lathyrism), cachexia,
CC   viral infections (hepatitis B and C), cancer and osteoporosis. The
CC   nucleic acid molecules are useful as probes, primers and chemical
CC   intermediates in biological assays, for constructing recombinant vectors,
CC   expressing antigenic portions of the protein. The peptide and nucleic
CC   acid sequences are useful as models for the development of human
CC   therapeutic targets, aid in the identification of therapeutic proteins
CC   and serve as targets for the development of human therapeutic agents that
CC   modulate kinase activity in cells and tissues that express the kinase.
CC   The host cells are useful in producing a kinase protein or peptide, and
CC   non-human transgenic animals. This sequence represents the human Ras-like
CC   protein of the invention
XX
SQ   Sequence 615 AA;

  Query Match             100.0%;  Score 3226;  DB 5;  Length 615;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-282;
  Matches  615;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRIFLMMHPWYIPSSQLAAKLLHIY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRIFLMMHPWYIPSSQLAAKLLHIY 60

Qy         61 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID 120

Qy        121 IDSVPTYKWKRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IDSVPTYKWKRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180

Qy        181 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF 240

Qy        241 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFR 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFR 300

Qy        301 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL 360

Qy        361 LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 420

Qy        421 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEM 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEM 480

Qy        481 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540

Qy        541 KDRLSVECRRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPPAIPLPAEIRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KDRLSVECRRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPPAIPLPAEIRE 600

Qy        601 EEVQTVEDGVFDIHL 615
              |||||||||||||||
Db        601 EEVQTVEDGVFDIHL 615
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AAW87995
ID   AAW87995 standard; protein; 609 AA.
XX
AC   AAW87995;
XX
DT   15-APR-1999  (first entry)
XX
DE   An alternatively spliced human MCG7 protein.
XX
KW   MCG4 protein; gene regulatory function; heat shock protein;
KW   guanine nucleotide exchange factor protein; MCG7 protein;
KW   heat shock-binding protein; MCG18 protein; zinc finger protein; cancer.
XX
OS   Homo sapiens.
XX
PN   WO9853061-A1.
XX
PD   26-NOV-1998.
XX
PF   22-MAY-1998;   98WO-AU000380.
XX
PR   23-MAY-1997;   97AU-00006972.
PR   23-MAY-1997;   97AU-00006973.
PR   23-MAY-1997;   97AU-00006974.
PR   22-JAN-1998;   98AU-00001458.
PR   22-JAN-1998;   98AU-00001459.
PR   22-JAN-1998;   98AU-00001460.
XX
PA   (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
XX
PI   Hayward N,  Silins G,  Grimmond S,  Gartside M,  Hancock J;
XX
DR   WPI; 1999-070146/06.
DR   N-PSDB; AAX04553.
XX
PT   New gene-expression regulatory genes, mcg4, mcg7, and mcg18 - encode a
PT   zinc finger protein, a GEF, and a heat shock or heat shock binding
PT   protein, useful to detect and treat cancer.
XX
PS   Claim 5; Fig 13b; 80pp; English.
XX
CC   The present sequence represents a MCG7 protein. The protein has gene
CC   regulatory functions, and has homology to a heat shock protein or heat
CC   shock-binding protein. The specification also describes MCG4, which is
CC   homologous to guanine nucleotide exchange factor protein, and MCG18,
CC   which is homologous to a zinc finger protein. Detection of mutations in
CC   the MCG genes can be used to identify the propensity for various types of
CC   cancer, and to treat, arrest, or otherwise ameliorate, the effects of a
CC   cancer in an animal or bird
XX
SQ   Sequence 609 AA;

  Query Match             98.6%;  Score 3180;  DB 2;  Length 609;
  Best Local Similarity   98.9%;  Pred. No. 3.3e-278;
  Matches  608;  Conservative    1;  Mismatches    0;  Indels    6;  Gaps    1;

Qy          1 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRIFLMMHPWYIPSSQLAAKLLHIY 60
              ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db          1 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRMFLMMHPWYIPSSQLAAKLLHIY 60

Qy         61 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID 120

Qy        121 IDSVPTYKWKRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IDSVPTYKWKRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180

Qy        181 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF 240

Qy        241 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFR 300
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFR 300

Qy        301 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL 360

Qy        361 LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 420

Qy        421 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEM 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEM 480

Qy        481 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        541 KDRLSVECRRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPPAIPLPAEIRE 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KDRLSVECRRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPP------EIRE 594

Qy        601 EEVQTVEDGVFDIHL 615
                |||||||||||||||
Db        595 EEVQTVEDGVFDIHL 609


RESULT 3
AAY70961
ID   AAY70961 standard; protein; 609 AA.
XX
AC   AAY70961;
XX
DT   09-AUG-2000  (first entry)
XX
DE   Human Ras signalling pathway associated protein CalDAG-GEFI.
XX
KW   Human; Ras signalling pathway; CalDAG-GEFI; calcium; DAG; diacylglycerol;
KW   GEF; guanine nucleotide exchange factor; RapIA; diagnosis; treatment;
KW   CalDAG-GEF-associated disorder; drug; transgenic animal model;
KW   Ras-associated cancer; protein therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          150. .173
FT                   /label= SCR1
FT                   /note= "Structurally conserved region which is highly
FT                   homologous to Ras-superfamily GEFs"
FT   Region          220. .262
FT                   /label= SCR2
FT                   /note= "Structurally conserved region which is highly
FT                   homologous to Ras-superfamily GEFs"
FT   Region          299. .320
FT                   /label= SCR3
FT                   /note= "Structurally conserved region which is highly
FT                   homologous to Ras-superfamily GEFs"
FT   Binding-site    433. .452
FT                   /label= EF-hand
FT                   /note= "calcium binding motif"
FT   Binding-site    499. .548
FT                   /label= DAG/phorbol_ester-binding_domain
FT                   /note= "present in most protein kinase C family members"
XX
PN   WO200024768-A2.
XX
PD   04-MAY-2000.
XX
PF   22-OCT-1999;   99WO-US024826.
XX
PR   23-OCT-1998;   98US-0105507P.
PR   16-NOV-1998;   98US-0108685P.
XX
PA   (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
PI   Kawasaki H,  Graybiel A,  Housman D;
XX
DR   WPI; 2000-350690/30.
DR   N-PSDB; AAD00311.
XX
PT   Isolated nucleic acid comprises nucleotide sequence encoding protein
PT   selected from normal or mutant CalDAG-guanine nucleotide exchange factor.
XX
PS   Claim 64; Page 90-92; 128pp; English.
XX
CC   The present sequence is a CalDAG-guanine nucleotide exchange factorI
CC   (GEFI) from a human frontal cortex and U937 lambdaZAPII cDNA libraries.
CC   The CalDAG-GEFI has substrate specificity for RapIA, dual binding domains
CC   for calcium and diacylglycerol (DAG) and highly expressed in brain,
CC   particularly in brain basal ganglia pathways and their axon-terminal
CC   regions. Expression of CalDAG-GEFI activates RaplA and inhibits Ras-
CC   dependent activation of the extracellular-signal regulated kinase/mitogen
CC   -activated protein (ERK/MAP) kinase cascade in 293T cells. The CalDAG-GEF
CC   proteins play an important role in determining the relative activation of
CC   Ras and Rap1 signalling induced by calcium and DAG mobilisation in brain
CC   and haematopoietic organs. The present sequence is used for diagnosis and
CC   treatment (by protein therapy) of CalDAG-GEF-associated disorders. It is
CC   also useful for developing drugs and producing cell-lines or transgenic
CC   animal models for Ras-associated cancers
XX
SQ   Sequence 609 AA;

  Query Match             98.6%;  Score 3180;  DB 3;  Length 609;
  Best Local Similarity   98.9%;  Pred. No. 3.3e-278;
  Matches  608;  Conservative    1;  Mismatches    0;  Indels    6;  Gaps    1;

Qy          1 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRIFLMMHPWYIPSSQLAAKLLHIY 60
                ||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db          1 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRMFLMMHPWYIPSSQLAAKLLHIY 60

Qy         61 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID 120

Qy        121 IDSVPTYKWKRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IDSVPTYKWKRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180

Qy        181 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF 240

Qy        241 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFR 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFR 300

Qy        301 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL 360

Qy        361 LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 420

Qy        421 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEM 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEM 480

Qy        481 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540

Qy        541 KDRLSVECRRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPPAIPLPAEIRE 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KDRLSVECRRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPP------EIRE 594
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